





cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances. \*

BASE COUNT	51 a	21 c	27 q	31 t
ORIGIN				
Alignment Scores:				
Pred. No.	1,01c.03			130
Score:	28.00			5
Percent Similarity:	100.00%			Conservative:
Best Local Similarity:	100.00%			Mismatches:
Query Match:	100.00%			Indels:
Gap:	12			Gaps:

US-09-856-070-26 (1-5) X BC19387 (1-130)

Qy 1 GlnAspTyrGluGlu 5  
          |||||  
Db 66 CAAGATTACCAAGAG 80

RESULT 4	
BG219430	
LOCUS	BG219430
DEFINITION	RST39188 Athersys RAGE
ACCESSION	BG219430
VERSION	BG219430.1 GI:13745451

Alignment Scores:	
Pred. No.:	1,01e+03
Score:	28.50
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	12
Length:	130
Matches:	5
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

115-09-856-070-26 (1-5) X H0219430 (1-130)

QY 1 ClnAspTyrGluGlu 5  
|||||  
LB 96 CAAAGATTGGAAGAG 80

RESULT 5  
BH719297/C

LOCUS	BM719297	136 bp	DNA	linear	CS5 20-FEB 2002
DEFINITION	BM636216	102,233 kb	Massive	Genomic clone	BM636216, DNA
					sequence.

Alignment Scores:	
Pred. No.:	1.08e+03
Score:	28.00
Length:	136
Matches:	5
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
DB:	17
Query Match:	100.00%
Best local Similarity:	100.00%
Percent Similarity:	100.00%
Pred. Score:	28.00

US-09-856-070-26 (1-5) x BH719297 (1-136)

QY 1 GlnAspTyrGluGlu 5  
|||||  
Ub 42 CAACAATTACAGCGAA 28

RESULT 6  
BG216901/C

LOC212901	137 bp	linear	EST: 21-APR 2001
PST36382	Athersys	RAGC Library	Homo sapiens CDNA, mRNA sequencing.
DEFINITION			

**SOURCE**  
HUMAN  
ORGANISM  
Homo sapiens  
Feketyota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates, Catarrhini, Hominoidea, Homo.  
1 (bases 1 to 137)

**REFERENCE**  
Harrington, J. J., Sherl, B., Pundlett, S., Jackson, P. D., Perry, P.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Jerner, E., Costanzo, B., McEligott, K., Hooper, S., Mays, R., Smith,  
E., Veloso, N., Kikla, A., Hess, J. J., Cotthren, K., Lo, K., Offenbacher

QY 1 GlnAspTyrGluGlu 5  
|||||  
Ub 42 CAACAATTACAGCGAA 28

RESULT 6  
BG216901/C

Accession	Gene	Library	Size (bp)	Accession	Gene	Library	Size (bp)
U02129	U2	U2	137	U02129	U2	U2	137
U02130	U3	U3	137	U02130	U3	U3	137
U02131	U4	U4	137	U02131	U4	U4	137
U02132	U5	U5	137	U02132	U5	U5	137
U02133	U6	U6	137	U02133	U6	U6	137
U02134	U7	U7	137	U02134	U7	U7	137
U02135	U8	U8	137	U02135	U8	U8	137
U02136	U9	U9	137	U02136	U9	U9	137
U02137	U10	U10	137	U02137	U10	U10	137
U02138	U11	U11	137	U02138	U11	U11	137
U02139	U12	U12	137	U02139	U12	U12	137
U02140	U13	U13	137	U02140	U13	U13	137
U02141	U14	U14	137	U02141	U14	U14	137
U02142	U15	U15	137	U02142	U15	U15	137
U02143	U16	U16	137	U02143	U16	U16	137
U02144	U17	U17	137	U02144	U17	U17	137
U02145	U18	U18	137	U02145	U18	U18	137
U02146	U19	U19	137	U02146	U19	U19	137
U02147	U20	U20	137	U02147	U20	U20	137
U02148	U21	U21	137	U02148	U21	U21	137
U02149	U22	U22	137	U02149	U22	U22	137
U02150	U23	U23	137	U02150	U23	U23	137
U02151	U24	U24	137	U02151	U24	U24	137
U02152	U25	U25	137	U02152	U25	U25	137
U02153	U26	U26	137	U02153	U26	U26	137
U02154	U27	U27	137	U02154	U27	U27	137
U02155	U28	U28	137	U02155	U28	U28	137
U02156	U29	U29	137	U02156	U29	U29	137
U02157	U30	U30	137	U02157	U30	U30	137
U02158	U31	U31	137	U02158	U31	U31	137
U02159	U32	U32	137	U02159	U32	U32	137
U02160	U33	U33	137	U02160	U33	U33	137
U02161	U34	U34	137	U02161	U34	U34	137
U02162	U35	U35	137	U02162	U35	U35	137
U02163	U36	U36	137	U02163	U36	U36	137
U02164	U37	U37	137	U02164	U37	U37	137
U02165	U38	U38	137	U02165	U38	U38	137
U02166	U39	U39	137	U02166	U39	U39	137
U02167	U40	U40	137	U02167	U40	U40	137
U02168	U41	U41	137	U02168	U41	U41	137
U02169	U42	U42	137	U02169	U42	U42	137
U02170	U43	U43	137	U02170	U43	U43	137
U02171	U44	U44	137	U02171	U44	U44	137
U02172	U45	U45	137	U02172	U45	U45	137
U02173	U46	U46	137	U02173	U46	U46	137
U02174	U47	U47	137	U02174	U47	U47	137
U02175	U48	U48	137	U02175	U48	U48	137
U02176	U49	U49	137	U021			

J., Danzig, J., and Ducar, M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 COMMENT  
 Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave., Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence stop: 139.  
 Location/Qualifiers  
 1..137  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

# FEATURES

source

BASE COUNT 33 a 31 c 23 g 50 t

ORIGIN

Alignment Scores:  
 Pred. No.: 1.09e+03 Length: 137  
 Score: 28.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-070-26 (1-5) x HG215901 (1-137)

QY 1 GlnAspTyrGluGlu 5  
 |||||  
 Db 72 CAGAGTACGAGAC 58

# RESULT 7

HG192394  
 LOCUS HG192394 139 bp mRNA linear EST 21-APR-2001  
 DEFINITION RST1508 Athersys PAGE Library Homo sapiens CDNA, mRNA sequence.  
 ACCESSION HG192394  
 VERSION HG192394.1 GI:13714081  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.  
 1 (bases 1 to 139)  
 Harrington, J., Sherf, R., Fundlett, S., Jackson, P.D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
 Lerner, L., Costanzo, D., McElligott, K., Beezer, S., Mays, R., Smith,  
 E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Ollenbacher,  
 J., Danzig, J., and Ducar, M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

# TITLE

JOURNAL  
 MEDLINE 21227151  
 COMMENT  
 Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave., Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence stop: 139.  
 Location/Qualifiers  
 1..139  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

# FEATURES

source

/clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

BASE COUNT 35 a 30 c 23 g 50 t

ORIGIN

# Alignment Scores:

Pred. No.: 1.11e+03 Length: 139  
 Score: 28.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-070-26 (1-5) x HG192394 (1-139)

QY 1 GlnAspTyrGluGlu 5  
 |||||  
 Db 74 CAGAGTACGAGAC 60

# RESULT 8

HG193988  
 LOCUS HG193988 139 bp mRNA linear EST 21-APR-2001  
 DEFINITION RST13140 Athersys PAGE Library Homo sapiens CDNA, mRNA sequence.  
 ACCESSION HG193988  
 VERSION HG193988.1 GI:13715675  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.  
 1 (bases 1 to 139)  
 Harrington, J., Sherf, R., Fundlett, S., Jackson, P.D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
 Lerner, L., Costanzo, D., McElligott, K., Beezer, S., Mays, R., Smith,  
 E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Ollenbacher,  
 J., Danzig, J., and Ducar, M.

# TITLE

JOURNAL  
 MEDLINE 21227151  
 COMMENT  
 Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave., Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence stop: 139.  
 Location/Qualifiers  
 1..139  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

# FEATURES

source

BASE COUNT 32 a 31 c 23 g 53 t

ORIGIN

# Alignment Scores:

Pred. No.: 1.11e+03 Length: 139  
 Score: 28.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0



US 09 856-070-26 (1-5) x B6170685 (1-148)

QY 1 GlnAspTyrGluGlu 5  
|||||

Db 36 CAGGATTATCAAGAA 50

# RESULT 11

LOCUS B6192932 154 bp mRNA Linear EST 21 APR 2002  
DEFINITION B6192932 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence  
ACCESSION B6192932  
VERSION B6192932.1 GI:13714619  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, K.,  
Cain, S., Iyenthal, C., Thornton, M., Ramachandran, R., Whittington, A.,  
Lerner, L., Costanzo, D., McEligott, K., Bouzer, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J., Danzig, J., and Bucar, M.

TITLE Creation of genome wide protein expression libraries using random  
activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 2127151

COMMENT Contact: Scott, J. Cain

Athersys, Inc.  
1201 Carnegie Ave., Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 461 9596

Email: scain@atersys.com

High quality sequence stop: 154.

# FEATURES

SOURCE

1..154

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Athersys RAGE Library"

/cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 62 a 24 c 30 q 38 t

# ALIGNMENT

Alignment Scores:  
Pred. No.: 1.28e-03 Length: 154  
Score: 28.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-070-26 (1-5) x B6192932 (1-154)

QY 1 GlnAspTyrGluGlu 5

|||||

Db 71 CAGGATTATCAAGAG 85

# RESULT 12

BM844888

LOCUS

DEFINITION K EST012404 STS25N0216 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BM844888  
VERSION BM844888.1 GI:19201287  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

# REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 157)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.F., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yusong-gu, Daegu 705-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yonasung@mail.kribb.re.kr

Plate: 93 row: F column: 08

High quality sequence stop: 157.

# FEATURES

SOURCE

1..157

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="ST25N0216-93-F08"

/sex="F"

/tissue\_type="lymph node"

/cell\_line="SNU-216"

/lab\_host="Top10F"

/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI;

Site\_2: NotI; The poly (A) RNA was diphosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated

with tobacco acid pyrophosphatase (TAP). The dephosphorylated

intact mRNA was ligated with DNA-RNA linker including EcoRI

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transfection of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 61 a 30 c 32 q 34 t

ORIGIN

1.31e-03 Length: 157

Score: 28.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0

US-09-856-070-26 (1-5) x BM844888 (1-157)

QY 1 GlnAspTyrGluGlu 5

|||||

Db 39 CAGGATTATCAAGAA 53

RESULT 13

AW867176

LOCUS

DEFINITION M1-SN0045-060400-001-q02 SN0035 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW867176

VERSION AW867176.1 GI:18201238

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 159)

## AUTHORS

Dias Neto, F., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, J.L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc Natl Acad Sci U.S.A. 97 (7). 3491-3496 (2000)

200202663

## MEDLINE

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FARESE/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=612-MPL-SN0045-060>)

400-001-402643=2000-04-0664-1)

Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence stop: 159.

## FEATURES

source

1..159

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="SN0045"

/dev\_stage="Adult"

/note="Organ: stomach; normal; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 59 a 40 c 29 g 41 t

ORIGIN

Alignment Scores:

Pred. No.: 1 34.03 Length: 159

Score: 28.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-856-070-26 (1-5) x AW867176 (1-159)

QY 1 GlnAspTyrGluGlu 5

|||||

DB 42 CAAGACTACGAGAA 59

RESULT 14

BI013708

164 bp mRNA linear EST 13-JUN-2001

LOCUS PM3-ET0207-230101-306-303 ET0207 Homo sapiens cDNA, mRNA sequence

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human

REFERENCE

AUTHORS

Dias Neto, F., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, J.L.F., de Souza, S.J. and

Simpson, A.J.

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

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Email: szhao@tiqar.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from ResGen (<http://www.resgen.com>). BAC end page: [http://www.tiqar.org/lib/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tiqar.org/lib/bac_ends/mouse/bac_end_intro.html)  
 Plate: 49 row: 1 column: 8  
 Seq primer: 17

Class: BAC ends.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-4918"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."  
 BASE COUNT 44 a 27 c 25 g 71 t  
 GCGGCG

Alignment Scores:  
 Pred. No.: 1.43e-03 Length: 167  
 Score: 28.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 17 Gaps: 0

US 09-856-070-26 (1-5) x A2227319 (1-167)

QY 1 GlnAspIyGlaGlu 5  
 |||||  
 DB 159 CAGGACTATGAGAA 145

Search completed: January 16, 2003, 21:37:14  
 Job time : 664.571 secs